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RAW SEQUENCE LISTING

DATE: 01/28/2002

PATENT APPLICATION: US/10/045,545

TIME: 14:08:53

Input Set : A:\U609811.app

Output Set: N:\CRF3\01282002\J045545.raw

PS

ENTERED

3 <110> APPLICANT: Maines, Mahin D.
 5 <120> TITLE OF INVENTION: METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
 6 TISSUE
 8 <130> FILE REFERENCE: 176/60981
 10 <140> CURRENT APPLICATION NUMBER: US/10/045,545
 11 <141> CURRENT FILING DATE: 2002-01-14
 13 <150> PRIOR APPLICATION NUMBER: 60/261,500
 14 <151> PRIOR FILING DATE: 2001-01-12
 16 <160> NUMBER OF SEQ ID NOS: 17
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 296
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Homo sapiens
 25 <400> SEQUENCE: 1
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 27 1 5 10 15
 29 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
 30 20 25 30
 32 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
 33 35 40 45
 35 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
 36 50 55 60
 38 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
 39 65 70 75 80
 41 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
 42 85 90 95
 44 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
 45 100 105 110
 47 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
 48 115 120 125
 50 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
 51 130 135 140
 53 Leu Leu Lys Gly Ser Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp
 54 145 150 155 160
 56 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
 57 165 170 175
 59 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
 60 180 185 190
 62 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
 63 195 200 205
 65 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
 66 210 215 220

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68 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
69 225                230                235                240
71 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
72                245                250                255
74 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
75                260                265                270
77 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
78                275                280                285
80 Gln Lys Tyr Cys Cys Ser Arg Lys
81 290                295
84 <210> SEQ ID NO: 2
85 <211> LENGTH: 1070
86 <212> TYPE: DNA
87 <213> ORGANISM: Homo sapiens
89 <400> SEQUENCE: 2
90 ggggtggcgc ccggagctgc acggagagcg tgcccgtcag tgaccgaaga agagaccaag 60
91 atgaatgcag agcccagag gaagtttggc gtggtggtgg ttggtggtgg ccgagccggc 120
92 tccgtgcgga tgagggactt gcggaatcca cacccttcct cagcgttcct gaacctgatt 180
93 ggcttcgtgt cgagaaggga gctcgggagc attgatggag tccagcagat ttctttggag 240
94 gatgctcttt ccagccaaga ggtggaggtc gcctatatct gcagtgaag ctccagccat 300
95 gaggactaca tcaggcagtt ccttaatgct ggcaagcacg tccttgtgga ataccccatg 360
96 aactgtcat tggcgccgc tcaggaactg tgggagctgg ctgagcagaa aggaaaagtc 420
97 ttgcacgagg agcatgttga actcttgatg gaggaattcg ctttcctgaa aaaagaagtg 480
98 gtggggaaaag acctgctgaa agggctgctc ctcttcacat ctgaccggtt ggaagaagac 540
99 cgttttggtt tccctgcatt cagcggcctc tctcgactga cctggctggt ctccctcttt 600
100 ggggagcttt ctcttggtgc tgccactttg gaagagcgaa aggaagatca gtatatgaaa 660
101 atgacagtgt gtcctggagac agagaagaaa agtccactgt catggattga agaaaaagga 720
102 cctggtctaa aacgaaacag atatttaagc ttccatttca agtctgggtc cttggagaat 780
103 gtgccaaatg taggagtga taagaacata tttctgaaag atcaaaatat atttgtccag 840
104 aaactcttgg gccagttctc tgagaaggaa ctggctgctg aaaagaaacg catcctgcac 900
105 tgcttggggc ttgcagaaga aatccagaaa tattgctgtt caaggaagta agaggaggag 960
106 gtgatgtagc acttccaaga tggcaccagc atttggttct tctcaagagt tgaccattat 1020
107 ctctattctt aaaattaaac atgttgggga aacaaaaaaaa aaaaaaaaaa 1070
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 296
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
115 <400> SEQUENCE: 3
116 Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
117 1 5 10 15
119 Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
120 20 25 30
122 Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
123 35 40 45
125 Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
126 50 55 60
128 Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
129 65 70 75 80
131 Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val

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132          85          90          95
134 Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
135          100          105          110
137 Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
138          115          120          125
140 Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
141          130          135          140
143 Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
144 145          150          155          160
146 Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
147          165          170          175
149 Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
150          180          185          190
152 Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
153          195          200          205
155 Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
156          210          215          220
158 Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
159 225          230          235          240
161 Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
162          245          250          255
164 Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
165          260          265          270
167 Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
168          275          280          285
170 Gln Lys Tyr Cys Cys Ser Arg Lys
171          290          295
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 295
176 <212> TYPE: PRT
177 <213> ORGANISM: Rattus norvegicus
179 <400> SEQUENCE: 4
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181 1 5 10 15
183 Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
184 20 25 30
186 Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
187 35 40 45
189 Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
190 50 55 60
192 Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu
193 65 70 75 80
195 Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu
196 85 90 95
198 Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu
199 100 105 110
201 Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu
202 115 120 125
204 Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu

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205      130      135      140
207 Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg
208 145      150      155      160
210 Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val
211      165      170      175
213 Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg
214      180      185      190
216 Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn
217      195      200      205
219 Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg
220      210      215      220
222 Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val
223 225      230      235      240
225 Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile
226      245      250      255
228 Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala
229      260      265      270
231 Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln
232      275      280      285
234 Lys Leu Cys His Gln Lys Lys
235      290      295
238 <210> SEQ ID NO: 5
239 <211> LENGTH: 1081
240 <212> TYPE: DNA
241 <213> ORGANISM: Rattus norvegicus
243 <400> SEQUENCE: 5
244 ggtcaacagc taagtgaagc catatccata gagagtttgt gccagtgcc caagatcctg 60
245 aacctctgtc tgtcttcgga cactgactga agagaccgag atggatgccg agccaaagag 120
246 gaaatttggg gtggtagtgg ttggtgttgg cagagctggc tcggtgaggc tgagggactt 180
247 gaaggatcca cgctctgcag cattcctgaa cctgattgga tttgtgtcca gacgagagct 240
248 tgggagcctt gatgaagtac ggcagatttc tttggaagat gctctccgaa gccaaagat 300
249 tgatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagtttct 360
250 gcaggctggc aagcatgtcc tcgtggaata ccccatgaca ctgtcatttg cggcggccca 420
251 ggagctgtgg gagctggccg cacagaaagg gagagtcctg catgaggagc acgtggaact 480
252 cttgatggag gaattcgaat tcctgagaag agaagtgttg gggaaagagc tactgaaagg 540
253 gtctcttcgc ttcacagcta gccactgga agaagagaga tttggcttcc ctgcgttcag 600
254 cggcatttct cgctgacct ggotggtctc cctcttcggg gagctttctc ttatttctgc 660
255 caccttgga ggcgaaaag aggatcagta tatgaaaatg accgtgcagc tggagacca 720
256 gaacaagggt ctgctgtcat ggattgaaga gaaagggcct ggcttaaaaa gaaacagata 780
257 tgtaaacctc cagttcactt ctgggtccct ggaggaagtg ccaagtgtag gggtaataa 840
258 gaacattttc ctgaaagatc aggatattt ttgtcagaag ctcttagacc aggtctctgc 900
259 agaggacctg gctgctgaga agaagcgcac catgcattgc ctggggctgg ccagcgacat 960
260 ccagaagctt tgccaccaga agaagtgaag aggaagcttc agagacttct gaagggggcc 1020
261 aggggtttgg cctatcaacc attcaccttt agctcttaca attaaacatg tcagataaac 1080
262 a 1081
265 <210> SEQ ID NO: 6
266 <211> LENGTH: 6
267 <212> TYPE: PRT
268 <213> ORGANISM: Artificial Sequence

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Input Set : A:\U609811.app

Output Set: N:\CRF3\01282002\J045545.raw

270 <220> FEATURE:
 271 <223> OTHER INFORMATION: Description of Artificial Sequence: hydrophobic
 272 domain of BVR
 274 <220> FEATURE:
 275 <221> NAME/KEY: PEPTIDE
 276 <222> LOCATION: (2)
 277 <223> OTHER INFORMATION: where X is any aa
 279 <400> SEQUENCE: 6
 280 Phe Xaa Val Val Val Val
 281 1 5
 284 <210> SEQ ID NO: 7
 285 <211> LENGTH: 6
 286 <212> TYPE: PRT
 287 <213> ORGANISM: Artificial Sequence
 289 <220> FEATURE:
 290 <223> OTHER INFORMATION: Description of Artificial Sequence: nucleotide
 291 binding domain of BVR
 293 <220> FEATURE:
 294 <221> NAME/KEY: PEPTIDE
 295 <222> LOCATION: (2)
 296 <223> OTHER INFORMATION: where X is any aa
 298 <220> FEATURE:
 299 <221> NAME/KEY: PEPTIDE
 300 <222> LOCATION: (4)..(5)
 301 <223> OTHER INFORMATION: where X is any aa
 303 <400> SEQUENCE: 7
 304 Gly Xaa Gly Xaa Xaa Gly
 305 1 5
 308 <210> SEQ ID NO: 8
 309 <211> LENGTH: 8
 310 <212> TYPE: PRT
 311 <213> ORGANISM: Artificial Sequence
 313 <220> FEATURE:
 314 <223> OTHER INFORMATION: Description of Artificial Sequence:
 315 oxidoreductase domain of BVR
 317 <400> SEQUENCE: 8
 318 Ala Gly Leu His Val Leu Val Glu
 319 1 5
 322 <210> SEQ ID NO: 9
 323 <211> LENGTH: 29
 324 <212> TYPE: PRT
 325 <213> ORGANISM: Artificial Sequence
 327 <220> FEATURE:
 328 <223> OTHER INFORMATION: Description of Artificial Sequence: leucine
 329 zipper of BVR
 331 <220> FEATURE:
 332 <221> NAME/KEY: PEPTIDE
 333 <222> LOCATION: (2)..(7)
 334 <223> OTHER INFORMATION: where X is any aa

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\U609811.app

Output Set: N:\CRF3\01282002\J045545.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:449 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:492 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17